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Range: from to ☐ Reverse complemented strand Features: ☐ SNP ☒ CDD

☐ 1: [NM_002771](#). Reports Homo sapiens prot...[gi:21536451]

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LOCUS NM_002771 807 bp mRNA linear PRI 27-NOV-2005
DEFINITION Homo sapiens protease, serine, 3 (mesotrypsin) (PRSS3), mRNA.
ACCESSION NM_002771 NM_007343
VERSION NM_002771.2 GI:21536451
KEYWORDS .
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Hominidae; Homo.
REFERENCE 1 (bases 1 to 807)
AUTHORS Marsit,C.J., Okpukpara,C., Danaee,H. and Kelsey,K.T.
TITLE Epigenetic silencing of the PRSS3 putative tumor suppressor gene in
non-small cell lung cancer
JOURNAL Mol. Carcinog. 44 (2), 146-150 (2005)
PUBMED [16013053](#)
REMARK GeneRIF: we determined the promoter hypermethylation status of
PRSS3 in a case series study of primary NSCLC, and found
methylation of this gene to be common, occurring in 53% (86 of 166)
of tumors examined.
REFERENCE 2 (bases 1 to 807)
AUTHORS Nemoda,Z., Teich,N., Hugenberg,C. and Sahin-Toth,M.
TITLE Genetic and biochemical characterization of the E32del polymorphism
in human mesotrypsinogen
JOURNAL FEBS Lett. 5 (2-3), 273-278 (2005)
PUBMED [15855826](#)
REMARK GeneRIF: The results classify E32del mesotrypsinogen as a frequent
polymorphic variant, which is not associated with chronic alcoholic
pancreatitis
REFERENCE 3 (bases 1 to 807)
AUTHORS Szmola,R., Kukor,Z. and Sahin-Toth,M.
TITLE Human mesotrypsin is a unique digestive protease specialized for
the degradation of trypsin inhibitors
JOURNAL J. Biol. Chem. 278 (49), 48580-48589 (2003)
PUBMED [14507909](#)
REMARK GeneRIF: biological function of human mesotrypsin is digestive
degradation of trypsin inhibitors
REFERENCE 4 (bases 1 to 807)
AUTHORS Katona,G., Berglund,G.I., Hajdu,J., Graf,L. and Szilagyi,L.
TITLE Crystal structure reveals basis for the inhibitor resistance of
human brain trypsin
JOURNAL J. Mol. Biol. 315 (5), 1209-1218 (2002)
PUBMED [11827488](#)

REMARK GenerIF: X-ray structure in complex with the inhibitor benzamidine at 1.7 A resolution; crystal structure reveals basis for inhibitor resistance

REFERENCE 5 (bases 1 to 807)
AUTHORS Nyaruhucha,C.N., Kito,M. and Fukuoka,S.I.
TITLE Identification and expression of the cDNA-encoding human mesotrypsin(ogen), an isoform of trypsin with inhibitor resistance
JOURNAL J. Biol. Chem. 272 (16), 10573-10578 (1997)
PUBMED 9099703

REFERENCE 6 (bases 1 to 807)
AUTHORS Stubbs,M.T., Huber,R. and Bode,W.
TITLE Crystal structures of factor Xa specific inhibitors in complex with trypsin: structural grounds for inhibition of factor Xa and selectivity against thrombin
JOURNAL FEBS Lett. 375 (1-2), 103-107 (1995)
PUBMED 7498454

REFERENCE 7 (bases 1 to 807)
AUTHORS Wiegand,U., Corbach,S., Minn,A., Kang,J. and Muller-Hill,B.
TITLE Cloning of the cDNA encoding human brain trypsinogen and characterization of its product
JOURNAL Gene 136 (1-2), 167-175 (1993)
PUBMED 8294000

REFERENCE 8 (bases 1 to 807)
AUTHORS Tani,T., Kawashima,I., Mita,K. and Takiguchi,Y.
TITLE Nucleotide sequence of the human pancreatic trypsinogen III cDNA
JOURNAL Nucleic Acids Res. 18 (6), 1631 (1990)
PUBMED 2326201

REFERENCE 9 (bases 1 to 807)
AUTHORS Rinderknecht,H., Renner,I.G., Abramson,S.B. and Carmack,C.
TITLE Mesotrypsin: a new inhibitor-resistant protease from a zymogen in human pancreatic tissue and fluid
JOURNAL Gastroenterology 86 (4), 681-692 (1984)
PUBMED 6698368

COMMENT REVIEWED REFSEQ: This record has been curated by NCBI staff. The reference sequence was derived from X15505.1.
On or before Dec 15, 2003 this sequence version replaced gi:20428774, gi:4506148.

Summary: This gene encodes a trypsinogen, which is a member of the trypsin family of serine proteases. This enzyme is expressed in the brain and pancreas and is resistant to common trypsin inhibitors. It is active on peptide linkages involving the carboxyl group of lysine or arginine. This gene is localized to the locus of T cell receptor beta variable orphans on chromosome 9. Additional transcript variants for this gene have been described, but their full length sequences have not been determined.
COMPLETENESS: complete on the 3' end.

FEATURES Location/Qualifiers

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ORIGIN

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